

Db 361 EISFISDVNNSSPALGTPPPWPGPPPTNFSSLEPQQVAKEGSPFAILLI 420
 Qy 421 GCVIAITLLLTIALMWRHLRHLRHLSKAERRVLEELTIVHLSVRQDTILINRGPRE 480
 Db 421 GCVIAITLLLTIALMWRHLRHLRHLSKAERRVLEELTIVHLSVRQDTILINRGPRE 480
 Qy 481 PPYQOERPRGMPHSAPCPVNGSALLISNPARYLIAATYARPPRGPPTPAWAKPTNT 540
 Db 481 PPYQOERPRGMPHSAPCPVNGSALLISNPARYLIAATYARPPRGPPTPAWAKPTNT 540
 Qy 541 QASGDYMEPEKGAPLIPPPQNSPVHYAEADIVTIVQVTGGNTAVPALPPGAVGDGP 600
 Db 541 QASGDYMEPEKGAPLIPPPQNSPVHYAEADIVTIVQVTGGNTAVPALPPGAVGDGP 600
 Qy 601 PRYDFPSRLRFREKLGQGEVHLCEDSPDOLYSLDFPLNVRKHPPLLYAVKLIRPD 660
 Db 601 PRYDFPSRLRFREKLGQGEVHLCEDSPDOLYSLDFPLNVRKHPPLLYAVKLIRPD 660
 Qy 661 ATKNASESLSFSENDELKEVKIMSRKLKDPTNIRLIGCVODDPCLMTDYMEGDLNQLS 720
 Db 661 ATKNASESLSFSENDELKEVKIMSRKLKDPTNIRLIGCVODDPCLMTDYMEGDLNQLS 720
 Qy 721 AHOLEDKRAEGARGDQGAQGTTISYPMLHQAQTASGMRYLATNFVRDLATRNLV 780
 Db 721 AHOLEDKRAEGARGDQGAQGTTISYPMLHQAQTASGMRYLATNFVRDLATRNLV 780
 Qy 715 AHOLEDKRAEGARGDQGAQGTTISYPMLHQAQTASGMRYLATNFVRDLATRNLV 774
 Db 715 AHOLEDKRAEGARGDQGAQGTTISYPMLHQAQTASGMRYLATNFVRDLATRNLV 774
 Qy 781 GENFTIKITADFGMSRNLYAGDYVRQGRAVLPIRWMACECLMGKFTTASDWAFGTVLW 840
 Db 775 GENFTIKITADFGMSRNLYAGDYVRQGRAVLPIRWMACECLMGKFTTASDWAFGTVLW 834
 Qy 841 EYLMCRAQPFQGQLTDEQVIENAGEFFRDQGRQVYLISRPPACPOGLYELMLRCWSRESEQ 900
 Db 835 EYLMCRAQPFQGQLTDEQVIENAGEFFRDQGRQVYLISRPPACPOGLYELMLRCWSRESEQ 894
 Qy 901 RPPFSQHLRFALDAALTVY 919
 Db 895 RPPFSQHLRFALDAALTVY 913

RESULT 2

A49508

protein-tyrosine kinase (EC 2.7.1.112) t_{rk}E precursor - human

C:Species: Homo sapiens (man)

C:Accession: A49508; 138358; 537402

J: Biol. Chem., B.; Cutulli, N.; Guarra, L.; Cancella, R.; De Luca, M.

A:Title: Molecular cloning of t_{rk}E, a novel t_{rk}-related putative tyrosine kinase receptor

A:Reference number: A49508; MUID:94043265

A:Accession: A49508

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-876 <DATA>

A:Cross-references: EMBL:X74979; PIDN:CA52915.1; PID:9400463

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-terminal homology <DNA> F; 30-185/Domain: discoidin I amino-terminal homology <DNA> F; 579-875/Domain: protein kinase homology <KIN> F; 579-587/Region: protein kinase Atp-binding motif

Query Match 94.5%; Score 4656.5; DB 2; Length 876;
 Best Local Similarity 95.3%; Pred. No. 8.1e-204; Indels 43; Gaps 2;
 Matches 876; Conservative 0; Mismatches 0; Indels 43; Gaps 2;

Qy 1 MCFEALSSLLLILVAVSGDADMKGHDPAKCRYALGMQDRITPDSIDASSSSWSDSTAAR 60
 Db 1 MCFEALSSLLLILVAVSGDADMKGHDPAKCRYALGMQDRITPDSIDASSSSWSDSTAAR 60

Qy 61 HSRLLESSDGDGAWCPCAGSVFVPREEEVQVDIQLRHLVALVGTOGRHAGGIGKFESRSYR 120
 Db 61 HSRLLESSDGDGAWCPCAGSVFVPREEEVQVDIQLRHLVALVGTOGRHAGGIGKFESRSYR 120

Qy 121 RYSRDRGRWMGMKDRWQEVISNEDPQGVVQKLDGPMPWVARYREVPRADRVMSVCLRV 180
 Db 121 RYSRDRGRWMGMKDRWQEVISNEDPQGVVQKLDGPMPWVARYREVPRADRVMSVCLRV 180
 Qy 181 ELYGCLWRDGLSYTAPVGQTMVLSSEAVYLNSTDYDGTIVGGIQLQYGGIQLADGVVGLD 240
 Db 181 ELYGCLWRDGLSYTAPVGQTMVLSSEAVYLNSTDYDGTIVGGIQLQYGGIQLADGVVGLD 240
 Qy 241 FRKSQELRWPGYDVGWSNHSPSGVYEMEFPFDRLRAFOAMQHVHNHMLGARLPG 300
 Db 241 FRKSQELRWPGYDVGWSNHSPSGVYEMEFPFDRLRAFOAMQHVHNHMLGARLPG 300
 Qy 301 VECPFRPGPAMWEGEPHRHNQGNGDPRARAVSPLGRLYARELOCRELAPGWILS 360
 Db 301 VECPFRPGPAMWEGEPHRHNQGNGDPRARAVSPLGRLYARELOCRELAPGWILS 360
 Qy 361 EISFISDVNNSSPALGTPPPWPGPPTNFSSLEPQQVKAEGSPFAILLI 420
 Db 361 EISFISDVNNSSPALGTPPPWPGPPTNFSSLEPQQVKAEGSPFAILLI 420
 Qy 421 GCVIAITLLLTIALMWRHLRHLRHLSKAERRVLEELTIVLVSVRQDTILINRGPRE 480
 Db 421 GCVIAITLLLTIALMWRHLRHLRHLSKAERRVLEELTIVLVSVRQDTILINRGPRE 480
 Qy 481 PPYQOERPRGMPHSAPCPVNGSALLISNPARYLIAATYARPPRGPPTPAWAKPTNT 540
 Db 481 PPYQOERPRGMPHSAPCPVNGSALLISNPARYLIAATYARPPRGPPTPAWAKPTNT 540
 Qy 505 - AVSGDYMEEPERGAPLIPPPQNSPVHYAEADIVTIVQVTGGNTAVPALPPGAVGDGP 563
 Db 505 - AVSGDYMEEPERGAPLIPPPQNSPVHYAEADIVTIVQVTGGNTAVPALPPGAVGDGP 563
 Qy 601 PRYDFPSRLRFREKLGQGEVHLCEDSPDOLYSLDFPLNVRKHPPLLYAVKLIRPD 660
 Db 601 PRYDFPSRLRFREKLGQGEVHLCEDSPDOLYSLDFPLNVRKHPPLLYAVKLIRPD 660
 Qy 661 ATKNASESLSFSENDELKEVKIMSRKLKDPTNIRLIGCVODDPCLMTDYMEGDLNQLS 720
 Db 661 ATKNASESLSFSENDELKEVKIMSRKLKDPTNIRLIGCVODDPCLMTDYMEGDLNQLS 720
 Qy 721 AHOLEDKRAEGARGDQGAQGTTISYPMLHQAQTASGMRYLATNFVRDLATRNLV 780
 Db 721 AHOLEDKRAEGARGDQGAQGTTISYPMLHQAQTASGMRYLATNFVRDLATRNLV 780
 Qy 781 GENFTIKITADFGMSRNLYAGDYVRQGRAVLPIRWMACECLMGKFTTASDWAFGTVLW 840
 Db 738 GENFTIKITADFGMSRNLYAGDYVRQGRAVLPIRWMACECLMGKFTTASDWAFGTVLW 797
 Qy 841 EYLMCRAQPFQGQLTDEQVIENAGEFFRDQGRQVYLISRPPACPOGLYELMLRCWSRESEQ 900
 Db 798 EYLMCRAQPFQGQLTDEQVIENAGEFFRDQGRQVYLISRPPACPOGLYELMLRCWSRESEQ 857
 Qy 901 RPPFSQHLRFALDAALTVY 919
 Db 858 RPPFSQHLRFALDAALTVY 876

RESULT 3

A53137

tyrosine kinase receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Accession: A53137; Tapley, P.; Saini, S.S.; He, B.; Pulido, D.; Barbacid, M.

A:Title: Multiple tyrosine protein Kinases in rat hippocampal neurons: Isolation of P

A:Reference number: A53137; MUID:94173920

A:Accession: A53137

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-910 <RES>

A:Cross-references: GB:L26525; PIDN:AA21099.1; PID:9432481

C:Genetics:

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-ter	Db	891	SQLHRLFLADALNTV
C;Keywords: ATP			
F;31-186/Domain: discoidin I amino-terminal homology <KIN>			
F;605-909/Domain: protein kinase homology <KIN>			
F;613-621/Region: protein kinase ATP-binding motif			
Query Match 92.9%; Score 4576.5; DB 2; Length 910;	RESULT	4	
Best Local Similarity 93.0%; Pred. No. 3.5e-200; Matches 836; Conservative 20; Mismatches 33; Indels 11; Gaps 3;	S42621		
1 MGREALSS-LILLIYASGDAADMKGHFPPAKRYCALGMDRTIPSDISASSSNSDSTA 59			
1 QY 1 MGCTGTLSLLLILVITGDADMKGHFPPAKRYCALGMDRTIPSDISASSSNSDSTA 59			
1 RHSRLESSDDGAWCPAGSVFVPEKEEYQVQDQLRHLHYALVGTQGRHAGGKGKRSR 119			
1 QY 60 RHRLESSDDGAWCPAGSVFVPEKEEYQVQDQLRHLHYALVGTQGRHAGGKGKRSR 119			
1 Db 61 RHRLESSDDGAWCPAGSVFVPEKEEYQVQDQLRHLHYALVGTQGRHAGGKGKRSR 120			
1 QY 120 LRYSDGRRRWMKDRNGQEVISGNEDPGVWLKGMDRTIPSDISASSSNSDSTA 179			
1 Db 121 LRYSDGRRRWMKDRNGQEVISGNEDPGVWLKGMDRTIPSDISASSSNSDSTA 180			
1 QY 180 VELYCILWRDGSLSYTAPVGQWMLSEAVYLNDSTYDGTIVGGLQYGGIGQOLADGVGLD 239			
1 Db 181 VELYCILWRDGSLSYTAPVGQWMLSEAVYLNDSTYDGTIVGGLQYGGIGQOLADGVGLD 240			
1 .QY 240 DFRKSQELRVWPGDYWGWSNHSFSSGVEMEFDRDRAFOAMQVMICNNMHLGARLG 299			
1 Db 241 DFRQSQELRVWPGDYWGWSNHSFSSGVEMEFDRDRAFOAMQVMICNNMHLGARLG 300			
1 QY 300 GVECRFRRGPAWGEPMRHNLLGGNLGDPRARAVSVPLGGRVARFGRVAFRFLQFAGPWL 359			
1 Db 301 GVECRFRRGPAWGEPMRHNLLGGNLGDPRARAVSVPLGGRVARFGRVAFRFLQFAGPWL 360			
1 QY 360 SEISFISDVNNSSPALGGTTPAPWHPGPPTNFSSLELPRQQPVAKAEGSPTAIL 419			
1 Db 361 SEISFISDVNNSSPALGGTTPAPWHPGPPTNFSSLELPRQQPVAKAEGSPTAIL 419			
1 QY 420 IGLCLVAIILLLIILALMWRHLWRRLISKAERRVLEELTLYHLSVQGDTIINNRGPR 479			
1 Db 417 IGLCLVAIILLLIILALMWRHLWRRLISKAERRVLEELTLYHLSVQGDTIINNRGPR 476			
1 QY 480 EPPYKOPPRPRGNPHSACPVNGSALLSNPAYRLLATYARPRPGPPPAAKPTN 539			
1 Db 477 EPPYKOPPRPRGTPTPSACPVNGSALLSNPAYRLLATYARPRPGPPPAAKPTN 536			
1 QY 540 TQAYSSDYMEEBKPGAPLPPPQNPNSVPHYEADIVTLQVIGGNTYAVPALPPGAVGD 599			
1 Db 537 TQACSDYMEBKPGAPLPPPQNPNSVPHYEADIVTLQVIGGNTYAVPALPPGAVGD 596			
1 QY 600 PPRVDPFRSLRFKEKLGEGOFGEVILCEVPSQDVLPSLDPFLNVRKGHLVAKTLP 659			
1 Db 597 PPRVDPFRSLRFKEKLGEGOFGEVILCEVPSQDVLPSLDPFLNVRKGHLVAKTLP 656			
1 QY 660 DATKNASFSLSRNDELKEVKIMSRKDPNIRLGLVCWQDPLCMITDYMENGDLQFL 719			
1 Db 657 DATKNA----RNDFLKEVKIMSRKDPNIRLGLVCWQDPLCMITDYMENGDLQFL 710			
1 QY 720 SAHQLEDKAARGAPGQGAQGPTISYPMLHVQAQIASHMRYLATLNFVRDLATNCL 779			
1 Db 711 SAHQLEDKAARGAPGQGAQGPTISYPMLHVQAQIASHMRYLATLNFVRDLATNCL 770			
1 QY 780 VGENFTIKIDFGMSRNLYAGDYVYRGRVYLTPRMAWEETLMGKFTTSDWAWGTYL 839			
1 Db 771 VGENFTIKIDFGMSRNLYAGDYVYRGRVYLTPRMAWEETLMGKFTTSDWAWGTYL 830			
1 QY 840 WEVMLCRACQPGQGLDEQVVIENAGEFFRQGRQVLSRSPACQPVLYEMLRCWRESE 899			
1 Db 831 WEVMLCRACQPGQGLDEQVVIENAGEFFRQGRQVLSRSPACQPVLYEMLRCWRESE 890			
1 QY 900 ORPPPSQLHRLAELNTV 919			
Query Match 48.8%; Score 2404; DB 2; Length 853;	RESULT	4	
Best Local Similarity 51.8%; Pred. No. 6.8e-102; Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;	S42621		
1 QY 3 PEALSLLILVASSGDAADMKGHFPPAKRYCALGMDRTIPSDISASSSNSDSTA 62			
1 Db 5 PRMLJVLFLPLS--SAKAQNPAAICRPILGKGGQIPDEDITASSQWSESTAKY 61			
1 QY 63 RLESSDGDAWCPAGSVFVPE-EELVQDQLRHLHYALVGTQGRHAGGKGKRSR 121			
1 Db 62 RLDSSEGDAWCPEIPVPEPDALKERFLQDIDLTHTLHTLVGQDPRHAGGKGIEFAMYKIN 121			
1 QY 122 YSRQRMRWQKDRNGQEVTSNEDPGVWLKGMDRTIPSDISASSSNSDSTA 181			
1 Db 122 YSRQRMRWQKDRNGQEVTSNEDPGVWLKGMDRTIPSDISASSSNSDSTA 181			
1 QY 182 LYGCILWRDGSLSYTAPVGQWML-SEAVYLNDSTYDGTIVGGLQYGGIGQOLADGVGLD 239			
1 Db 182 LYGCILWRDGSLSYTAPVGQWML-SEAVYLNDSTYDGTIVGGLQYGGIGQOLADGVGLD 240			
1 QY 240 DFRKSQELRVWPGDYWGWSNHSFSSGVEMEFDRDRAFOAMQVMICNNMHLGARLG 299			
1 Db 241 DFRQSQELRVWPGDYWGWSNHSFSSGVEMEFDRDRAFOAMQVMICNNMHLGARLG 300			
1 QY 300 GVECRFRRGPAWGEPMRHNLLGGNLGDPRARAVSVPLGGRVARFGRVAFRFLQFAGPWL 359			
1 Db 301 GVECRFRRGPAWGEPMRHNLLGGNLGDPRARAVSVPLGGRVARFGRVAFRFLQFAGPWL 359			
1 QY 360 SETSFISD-VWNNSPALGGTTPAPWHPGPPTNFSSLELPRGGDQPVAKAEGSPTAI 418			
1 Db 360 SETSFISD-VWNNSPALGGTTPAPWHPGPPTNFSSLELPRGGDQPVAKAEGSPTAI 400			
1 QY 419 IGLCLVAIILLLIILALMWRHLWRRLISKAERRVLEELTLYHLSVQGDTIINR 476			
1 Db 401 IGLCLVAIILLLIILALMWRHLWRRLISKAERRVLEELTLYHLSVQGDTIINR 476			
1 QY 477 GPRP-----PPQYKOPPRPRGNPHSACPVNGSALLSNPAYRLLATYARP 523			
1 Db 461 SPSEQQSNSTYDRIFPLRDYQSP-----SPLRKIPEF----- 494			
1 QY 524 PRGPPPTPAWAKPTNTQASGSDYMEPEKPGAPLPPPQNPNSVPHYEADIVLQVIGG 583			
1 Db 495 -----APGEEESGCSCGVKPVQPSG-----EGVPHYAEDIVLNQVIGG 535			
1 QY 584 NTYAVPALPPGAVGDPGPYR-----PPRSRSLRFKEKLGEGOFGEVHLCEVMEGERFKDIDFAL 642			
1 Db 536 NTYSVAPTMIDLGSKDVAVEEPRKLTFKEKLGEGOFGEVHLCEVMEGERFKDIDFAL 595			

QY 643 NVRKGHPLLVAKTILRDPATKNAEFSLEFRNDEKEVKNSRKDPNTRLGLGVQDPP 702
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 596 DVSANOPVLYAVKMLRADANKA-----RNDFLKEIKIMSRKDNPNTIHLSSVCITDD 649

QY 703 LCMTDYMEGNDLNOFLSAHOLEKKAECAPGQQAQOPTIVPMUHVAAQIASGRY 762
Db ||||:|||||:|||||:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 650 LCMTEYMEGNDLNOFLSRE-----PPNSSSDVRTSYTNUKEMATOJIASGRY 700

QY 763 LATLNFVRHDLATRNCLVGENTFTIKIADFGMSRNLYAGDYYRVRGRAVLPIRRAWECTL 822
Db ||:|||||:|||||:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 701 LSLSNFVRHDLATRNCLVGNTIKIADFGMSRNLYGDYRGRALVPIRMWSIL 760

QY 823 MGKFNTASDWAFAGTYLWETUMLCRAQPGQOLIDEQEVENAGFPRDGROVULSRPAC 882
Db 761 LGKFTTASDWAFAGTYLWETFPQEQPQLSDEQVIENTGFERDQGQTLQPAIC 820

QY 883 PQGLVELMLCWCSESEQRPPSOLHRLAE 913
Db 821 PDSVYKLMSCWRRTDKNRPSPQEIHLILQ 851

RESULT 5

148859 tyro 10 receptor kinase - mouse
C;Species: Mus musculus (house mouse)
C;Accession: 02-Jul-1995 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
R;Lai, C.; Lemke, G.
Oncoene 9, 877-883, 1994
A;Title: Structure and expression of the Tyro 10 receptor tyrosine kinase.
A;Reference number: 148859; MUID:94151011
A;Accession: I48859
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-819 <RES>
A;Cross-references: EMBL:X76505; NID:9435161; PID:9435162
C;Genetics:
A;Gene: tyro 10
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP
F;534-542/Region: protein kinase ATP-binding motif

Query Match 47.5%; Score 2341; DB 2; Length 819;
Best Local Similarity 52.1%; Pred. No. 4.6e-99; Matches 465; Conservative 116; Mismatches 208; Indels 104; Gaps 15;

QY 42 IPDSDISASSSWSDSTAARHSRLESSDDGAWKPGASTPKEEYQVQDYLRLHLYALV 100
Db 6 IPDEDITASSQWSPSTAATKGRDSEEGDGAWEPEIPVQPDQDDLFKLDRLTILHFTLV 65

QY 101 GTDERRHAGGKGKERSRSYLYRVDGRGMWDRMGEVISONESENPDGVWIKLKGPMW 160
Db 66 GTQSHHAGGKGKERSRSYLYRVDGRGMWDRMGEVISONESENPDGVWIKLKGPMW 125

QY 161 ARVRFYPRADRVWSVCLRELVGLCWDRGLSLTAPVQGQMTI--SRAVYIINDSTDGH 218
Db 126 ARFVRLIPVTDHSINVCMVRLGGCWVQDGLSYNAPQOFLPGGSIIYIINDSVPG- 184

QY 219 TGGGLQYQGGQLADGWGLDRRSQELRVWGYDVGWSNSFSSCYVEMEFERLR 278
Db 185 AVGISMTEGIGQLQDGDVSGLDDFTOTHEHVVWGYDYGWWRNEASATINGFIEINFEFDIR 244

QY 279 AFOAMQHQNMMHILGARLPGYCECRERGPAWEGPMRHLLGGNGDPRARAVSPL 338
Db 245 NFTPKVHNMFANGVKFKKEYQCYF-RSEASEBEPATAVYFPLDQDNPSRFVTPVPL 303

QY 339 GGRRARFLOCREFLAGPWLFSEISFISD--VNINSSPALGGTFPPAWWWPPCPPTNFS 396
Db 304 HHRMASAIKCOYHFADTWMSFELTFOODAMMNNS---GALPTSP----- 346

QY 397 SLELEPROSQOPVAKAEGSPTAILGCLVAILLLLITALMLWRLHWRLLSKAERRVYLE 456

RESULT 6

180329 receptor tyrosine kinase - rat (fragment)
C;Species: Rattus sp. (rat)
C;Accession: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Sep-1999
C;Status: preliminary; translated from GB/EMBL/DDBJ
R;Sakuma, S.; Sayo, H.; Iijichi, A.; Tofilon, P.J.
Radiat. Res. 143, 1-7, 1995
A;Title: Radiation induction of the receptor tyrosine kinase gene Ptk-3 in normal rat
A;Reference number: I59442; MUID:95320273

QY 801 DYRYQVGRAVLPIRMWAECEILQMGKFTTASDWAFAGYVILWEMLCRQPGFQLTDEOVI 860
Db 703 DYRIQGRVLPTRWMSHESILGKFTTASDWAFAGYVILWEMLCRQPGFQLTDEOVI 762

QY 861 ENAGEFFPRDQGROYLSRPACPOGLYELMRLROWSRESEQRPPFSQURFLAE 913
Db 763 ENTCGEFFRQGQIYLPOPALCPDSVYKLMSCWRRETKHRPSFQEIHLLQ 815

Query Match 23.5%; Score 1159; DB 2; Length 220;
Best Local Similarity 98.6%; Pred. No. 4e-46; Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 404 GOOPVAKARGSPAPLIGLCLVATILLILIAMLWRLHWRLLSKAERRVLEELVHL 463
Db 1 GOOPVAKARGSPAPLIGLCLVATILLILIAMLWRLHWRLLSKAERRVLEELVHL 60

QY 464 SVGDTILINNRGPREPQYQFPRPRNPNSAPCUPNGSALLSVPAYRLLATYARP 523
Db 61 SVGDTILINNRGPREPQYQFPRPRNPNSAPCUPNGSALLSVPAYRLLATYARP 120

QY 524 PRGPGPPTPAWAKPTNTQAVYSGDYMEEPKPGABLPPPPQNSVPHYAEDATVLOGVTG 583
Db 121 PRGPGPPTPAWAKPTNTQACSGDYMEEPKPGABLPPPPQNSVPHYAEDATVLOGVTG 180

QY 584 NTYAVPAPLPGAVGDPGPPRVDPPRSRLRFKRLGEGOFGE 623

Db	181	NTYAVPALPPGAVDGDPPIVDFPSSLRLFKLGEQFGE	220
RESULT	7		
T16031		hypothetical protein F11D5.3 - <i>Caenorhabditis elegans</i>	
C;Species:		<i>Caenorhabditis elegans</i>	
C;Date:	20-Sep-1999	#sequence_revision 20-Sep-1999 #text_change 24-Nov-1999	
C;Accession:	T16031		
R;Ntnan, M.			
A;submitted to the EMBL Data Library:		November 1995	
A;Description:	The sequence of <i>C. elegans</i> cosmid F11D5.		
A;Reference number:	218449		
A;Gene:	CESP:F11D5	3	
A;Status:	preliminary; translated from GB/EMBL/DDBJ		
A;Molecule type:	DNA		
A;Residues:	1-791 <NHA>		
A;Cross-references:	EMBL:U41532; NID:91118032; PID:91118035; PIDN:AAA83276.1; CESP:F11D5		
C;Genetics:			
A;Introns:	52/2; 85/1; 129/3; 179/1; 275/3; 380/1; 469/2; 493/2; 569/1; 612/2; 638/2; 74		
C;superfamily:	unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog		
Query Match	19 %;	Score 969; DB 2; Length 791;	
Best Local Similarity	28.3 %;	Pred. No. 5.5e-37;	
Matches	254;	Conservative	150;
Db	46	DIASSSSWSDSTAAR-HSLESGSGDAGNCAGCAGPAGSVPKEREYLQDQLQRHLVALVGCG	104
Qy	105	RHAGGLGEKFPSVYRLRSRQD RRMGKDRWQEVISNEDPEGVWKLQLGPPMVAI	163
Db	94	RFDGGHMEYATKAIIKQWPLSNLAWASKTIDELTIAANDETAHAIIRHLDRIIARR	153
Qy	164	VRYTPRADDVMSVCLRVETYGCLMRDGLSYTAPVGQTMWLSAEVYLNSTYDGHVGG	223
Db	154	IRIVPVSHSTRTVCMRVEFGCPFPDSLVLFYINVDQGD--LQSISYHDFSYDGNLANS	210
Qy	224	QY-GGLSGLADGVYGLDFFRKSQSLBLRVNGYDVGWSNHSFSSGYVEMFEDRRAFA	282
Db	211	HLTGGIGKILDGEGVKNNVFVNH-----HKWVGWRRK-RNGNVKLAPEFSELNTSG	261
Qy	283	MQVHCNHNHTL GARLPGCVERRRRGPMAMWEGSPMRHLLG-----NLGPR---	330
Db	262	LIHTSN-----ERKKS-AKFSATVYLISINGKDFSTDTHENPDTES	306
Qy	331	--ARAVSVPLGGRVAFQLCREFLA-GFWLFLSEISFTSDVNN--NSSPALGGTFPP	382
Db	307	EYPRWIRIPPNRIRAKYAKIRLNFGTOSDWLFESEVNFSKHNIELNDVVIT----	360
Qy	383	ARWWPPGPPTPTTNSLELEP560QVPAKAEKGSTAILIGCLVIIIILLIATMLWRLH	442
Db	361	-----PDVSYSFVSTBHDGT-----SMFAFI-FFFMLIVAVILTVLYRK	403
Qy	443	WRLLS---KAERYLLEELVHLSYPGDTLILINNRGPRREPPPQEPFRPRGNPNSA	497
Db	404	EVVKASSPPSPNAREL-----LTDGNTKHH---YSPSTIQMAR-----	442
Qy	498	PCVPNGSALLSNPAVLLATYARPPRGPPPTPAWAKPTNT-QAYSGDMEPEKG	554
Db	443	--DNLQLNATEKMPMSPIISDYAEPDISVCSDTA----NPPLIGDGPY-DTQKRS	493
Qy	555	APLLPPPQQNSVPHAYRADIVLTLQGVGGNTAVPALPPGAVGDGPPRDFPSSLRLFK	614
Db	494	NPL-----SSAVKVYSD-----GEVYCT-TLP-----EIAKDKLICVS	525
Qy	615	KLGEGFGEVHLCVESSQPODEVSLDFPLNVRKGHLVAKVKTLPDATKNAFSLSFRND	674
Db	526	RIGQGFGEVDLQLEN-----RK-----VAKKLH-----GISQADEFS	560
RESULT	8		
A44547		receptor tyrosine kinase Xtrk - African clawed frog (fragment)	
C;Species:	Xenopus laevis (African clawed frog)		
C;Date:	31-Dec-1993	#sequence_revision 31-Dec-1993 #text_change 10-Sep-1997	
C;Accession:	A44547		
R;Kelman, Z.		submitted to the Protein Sequence Database, December 1993	
A;Reference number:	A44547		
A;Accession:	A44547		
A;Status:	preliminary; not compared with conceptual translation		
A;Molecule type:	mRNA		
A;Residues:	1-248 <KEL>		
C;Superfamily:	unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology (fragment) <RIN> F,1-246/Domain: protein kinase homology (fragment) <RIN>		
Query Match	19.5 %;	Score 963; DB 2; Length 248;	
Best Local Similarity	72.6 %;	Pred. No. 3.3e-37;	
Matches	175;	Conservative	28;
Db	668	SIFSRNFILKEVKIMRSKUDPNTRLIGCVODDPLOMIDYNGENLSNQFLSAHOLEDK	727
Qy	2	SISSNSPLKEKILSKLSDPAPLRLIGACDDEDPLGMITEMENGDLNQFLSSHHDE	61
Db	728	AAEGAPGDQAOAQOPTISYPMLHVQAQIASGMRVLAATLNFVHDLATRNCLVGENFTIK	787
Qy	62	EENG-----AHCLPATSYSSLLHVHALQICSGMKYLLSLNFVHDLASRNCLVGENFTIK	115
Db	788	IADFMSRNLYAGDVYRQVGRALVPIRMMACELINGKFTTASDWWAFGVVILWEVLMCR	847
Qy	116	IADFMSRNLYAGDVYRQVGRALVPIRMMACELINGKFTTASDWWAFGVVILWEVLMCR	175
Db	848	AQPFGQIJDQEVIENAGEFFRDQGQVYLSRPPACQPGYELMRCWSREBQPRPSQL	907
Qy	176	EQPYGEELSDEVIEANGELFUDSKKQIFLFRPPCQOPLYELMAQWSRDERERPSFQDI	235
Db	236	H 236	
RESULT	9		
159442		receptor tyrosine kinase - rat (fragment)	
C;Species:	Rattus sp. (rat)		
C;Date:	02-Aug-1996	#sequence_revision 02-Aug-1996 #text_change 24-Sep-1999	
C;Accession:	I59442		
R;Salama, S.; Soya, H.; Ijichi, A.; Tofilon, P.J.			
Radiat. Res. 143, 1-7, 1995			
A;Title:	Radiation induction of the receptor tyrosine kinase gene Ptk-3 in normal rat		
A;Reference number:	I59442; MUID:95320273		
A;Accession:	I59442		
A;Status:	preliminary; translated from GB/EMBL/DDBJ		
A;Molecule type:	mRNA		

F:92-115 /Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:116-138 /Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:139-150 /Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
 F:452-821 /Domain: cytosolic #status predicted <CTY>
 F:535-813 /Domain: protein kinase homology <KIN>
 F:543-551 /Region: protein kinase AMP-binding motif
 F:67-95,121-178,205,241,254,280,325,338,350,411 /Binding site: carbohydrate (Asn) (covalent)
 F:571 /Active site: Lys #status predicted
 F:701 /Binding site: phosphate (Tyr) (covalent) #status predicted
 F:816 /Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match Best Local Similarity 30.1%; Score 648.5; DB 1; Length 821; Matches 201; Conservative 72; Mismatches 186; Indels 207; Gaps 23;

Oy 373 SPALGSIFPPPAFWKWPCCPPTFSSLELPSCQQPVKAEGSPTAILGLVAVILLL 432
 217 SCSVGGDPLPTLWWDVNVLVKHMNETSHTOQSLRNTISDDSGKOISCV----- 267

Oy 433 LIALMLARLHWKRLLSKAERRVLEERETVHLSW--PGDTIINNRPGPREP----- 482
 Db 268 -----AENIUVGEDQDSVNLTWHRAPITFL-----ESFTSDHHWC 302

Oy 483 -PYQEPRPRGNGNPHSAACPVCVNGC-----ALLSNPA-----Y 513
 Db 303 IPRF--TVRGAIKPALQWFYNGALNESKYICKTKIRHTNHTEYHGCLQDNPPTHMNNGDY 359

Oy 514 RULL-----ATVAPRPRGPGPPTPAWAKPTNQAYSCDYMEE-E 551
 Db 360 TLMKNEYGKDERQIQIAHFMGRGPVGYETNPVNPYPEVLYEDWNTPTDI---GDTNKSNE 415

Oy 552 KPGAPLLPPIPQNSPVPHYAEDIVTQGV----- 580

Db 416 IPSTDYADQTNRHELSVYAVVVTASYWGFCLVWMLILKLARRHSKGGMKGPAVISNUDD 475

Oy 581 -----TGTNTYAVPALPPGAVGDGP---PRVDFP-----RS 608

Db 476 SASPLHHSNSNTPSSEGGPPDAVIGMTKIPVIENPOYFGITNSQLKPDFTWQHTRH 535

Oy 609 RLRFKIKLGEOFGEPHLCE---VSQDPLVSLDFPLANVRKGPHLAVAKTLRPDTAKNA 665

Db 536 NIVLKRELGEAGFAFKVFLAEYCYNLCPEQD-----KILWAVKTIK-DASDNA 580

Oy 666 SEFSLSRNDELKEVKIMSRAKDPPNITRLGLCVQDQPLCMTDYMEGDLNQFLSAHOLE 725

Db 581 -----RKDFHREALELTNLQHEHTVKFYGVCGVEGSDPLIMFYMHGDLKFLRAHGP 634

Oy 726 D-KAAEGAPGPGQQAQGPT-ISYPMILHVAAQIASGMYLATLNFVHRLDAINTRCLVGEN 783

Db 635 AVLMAEGNP-----PTELTQSOMHLHQIQIAQMGVYLASQHFVHRLDAINTRCLVGEN 686

Oy 784 FTIKIADFGMSRNLAQDGYYRVQGRAVLPTWMANICILMKFTTAQDWAQFGVTLWEVL 843

Db 687 LLVKIGDFGMSRVDVISTDYIRVGHTMLPIRWMPPESIMRKFETESDVNSLGVVWEIF 746

Oy 844 MLCRQPFQGQLTDEQVIEVANEAGEFFRDQGRQYLSRSPACTPOGLYELMLRCWSRSEQRQP 903

Db 747 TYK-GQWQLSNEVIECI----TQGR--VLQRPRTCPOQEYELMLGCWOREPHTRN 798

Oy 904 FSQLHRFL 911

Db 799 IKNIHTLL 806

RESULT 12

S44058 brain-derived neurotrophic factor receptor precursor - chicken
 N; Alternate names: receptor tyrosine kinase trkB
 N; Contains: protein-tyrosine kinase (EC 2.7.1.112)
 C; species: Gallus gallus (chicken)
 C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999

C; Accession: S55939; S42175; S44098
 R; Vinh, N.Q.; Erdmann, K.S.; Heumann, R.
 Gene 149, 383-384, 1994
 A; Title: Cloning and sequence analysis of a cDNA encoding a novel truncated form of
 F:452-821 /Domain: cytosolic #status predicted <CTY>
 F:535-813 /Domain: protein kinase homology <KIN>
 F:543-551 /Region: protein kinase AMP-binding motif
 F:67-95,121-178,205,241,254,280,325,338,350,411 /Binding site: carbohydrate (Asn) (covalent)
 F:571 /Active site: Lys #status predicted
 F:701 /Binding site: phosphate (Tyr) (covalent) #status predicted
 F:816 /Binding site: phosphate (Tyr) (covalent) #status predicted

A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994
 R; Becham, G.; Blifo, S.; Ozawa, H.; Kolbeck, R.; Pottgiesser, J.; Barde, Y.A.
 Development 119, 545-558, 1993
 A; Title: Expression and binding characteristics of the BDNF receptor chick trkB.
 A; Cross-references: EMBL:X77251; NID:9563881; PIDN:CAA54468.1; PID:9472934
 A; Reference number: S42175; MUID:94116452

A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-818 <DEC>
 A; Cross-references: EMBL:X74109; NID:9407798; PIDN:CAA52210.1; PID:9407799
 A; Genetics:
 A; Gene: trkB
 C; Function:
 A; Description: regulation of nervous system development; receptor for brain-derived
 C; Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-gly
 A; Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth fac
 Inse
 F:1-31 /Domain: signal sequence #status predicted <SIG>
 F:32-818 /Product: brain-derived neurotrophic factor receptor #status predicted <CAT>
 F:32-432 /Domain: extracellular #status predicted <EXT>
 F:33-90 /Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:91-114 /Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:115-137 /Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:138-149 /Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical
 F:433-449 /Domain: transmembrane #status predicted <TM>
 F:450-818 /Domain: cytosolic #status predicted <CTY>
 F:532-810 /Domain: protein kinase homology <KIN>
 F:540-548 /Region: protein kinase AMP-binding motif
 F:56, 94, 120-199, 204, 253, 287, 324, 337, 349, 408 /Binding site: carbohydrate (Asn) (covalent)
 F:568 /Active site: Lys #status predicted
 F:813 /Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
 F:813 /Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match Best Local Similarity 34.2%; Score 648; DB 1; Length 818; Matches 176; Conservative 71; Mismatches 149; Indels 118; Gaps 19;

Oy 446 LLSKAERVLREBLTVH-LSVPGDTIILNRPGRPPPPYQCB---PRPRGNPPH---- 495
 Db 360 LIAKNEGEDEKRVDAAHFMSPGQD----GSGPITVDPVVEYETTFNDLGDTTNSNQI 413

Oy 496 SARCVPG-----SALLSNPARYLIAVAPP-----RGCPPTPAWAKP 537

Db 414 ISPDVSNKEEDSITVWVVGTAALVCTGTYLMLILIKFRGHSKFGMKG----- 463

Oy 538 TMQAYSGDYMPEKEFGAPLLPPPQNSPVPHYAEDIVTQGVGIGTYAVPALPPGAVG 597

Db 464 -SSVTSND---DDPASPL-----HIIISNSNTSSSEGPDAVIGMTKIPV 507

Oy 598 DGPPRYDFPFSRLR-----FKEKLGEQFGEPHLCE---VSQDPLVSLDF 640

Db 508 ENPQYFGITNSQLKPKTFVQHVKRHNIVKLRLGEAGFAFKVFLAEYCYNLCPEQD---- 561

Oy 641 PLNVRKGPHPLIVAVKLRLPDKTNAFSLSLRSRNDLKEVKIMSRAKDPNITRLGLCVQD 700

Db 562 -----KILWAVKTIK-DASDNA-----RKDFHREALELTNLQHEHTVKFYGVCG 606

Oy 701 DPLCMITDYMENGDLNQFLSAHQELODKAEGAPGQGAQG--PTISVMLHVQTA 757

Db 607 DPLIMFEYMHGDLKFLRAH-----GPDVTLMAQGRPAELTOSQMLHAQPA 657

Oy 758 SGMYLIALTNFVRDLATRCLVGENFTIKIADFGMSRNLYAGDYYRVOGRAVLPIRWA 817

Db 658 AGMYLTLASQHVFVRDLATRNCLVGENLILVKIGDGMRSRDVYSTDYRVGHTMLPIRWP 717
 Qy 818 WECIMGKTTASDWAWGVTLINEVLMCRAQFGQLDQEVENAGEFRDQGRQVLS 877
 Db 718 PESTMYKTTESDWSLGVNLNEVTECI----TQGR--VLR 769
 Qy 878 RPPACPOGYELMURCWSRESEQRPPFSOLHRL 911
 Db 770 RPRCPKEVYDLMGCGWOREPHMRNLKEIHSIL 803

RESULT 13
 A5653 brain-derived neurotrophic factor receptor precursor - human
 N;Alternate names: receptor tyrosin kinase trkB
 N;Contains: protein-tirosine kinase (EC 2.7.1.112)
 C;Species: Homo sapiens (man)
 C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 11-Jun-1999
 C;Accession: A5653; I16557
 C;Molecule type: mRNA
 A;Residues: I-822 <NAK>
 A;Cross-references: GB:U12140; NID:9525313; PIDN: AAC51371.1; PID:9530791
 R;Shelton, D.L.; Sutherland, J.; Gripp, J.; Camerato, T.; Armanini, M.P.; Phillips, H.S.;
 J. Neurosci. 15, 477-481, 1995
 A;Title: Human trks: molecular cloning, tissue distribution, and expression of extracellular
 A;Reference number: 150557; MUID:95123473
 A;Accession: 156557
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Residues: I-822 <SHE>
 C;Genetics:
 A;Gene: GDB:WTRK2; trkB
 A;Cross-references: GDB:122898; OMIM: 600456
 A;Map position: 9q22.1-9q22.1
 C;Function:
 A;Description: regulation of nervous system development; receptor for brain-derived neurotrophic factor
 C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
 gene
 F1-31/Domain: signal sequence #status predicted <SG>
 F1-32-82/Domain: brain-derived neurotrophic factor receptor #status predicted <MM>
 F1-2-435/Domain: extracellular #status predicted
 F1-61/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
 F1-92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
 F1-116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F1-139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
 F1-436-452/Domain: transmembrane #status predicted <TM>
 F1-453-814/Domain: cytosolic #status predicted <CYT>
 F1-544-552/Region: protein kinase homology <KIN>
 F1-67,95-121-178,205,241,254,280,325,338,350,412/Binding site: carbohydrate (Asn) (covalent
 F1-572/Active site: Lys #status predicted <ATP>
 F1-706/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 F1-817/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 13.1%; Score 645.; DB 1; Length 822;
 Best Local Similarity 46.5%; Pred. No. 2_6e-22;
 Matches 144; Conservative 45; Mismatches 79; Indels 42; Gaps 10;

Db 580 NA-----RKDFHREAELTNLQHEHIVKFYGVCEGDLJMVPEYMKHGDLNKFRLAIG 633
 Qy 724 LED-KAEGARGDGOAQPT-ISPMPLHLVAQTASGRMLVATNFVRDLATRNCLV 781
 Db 634 PDAVIMAEQNP-----PTELTOSOMHQAQTAQGMYLTLASQHVFVRDLATRNCLV 685
 Qy 782 ENFTKIAFDGMSRNLYAGDYRYVQGRAVAPIRMAWECIMGKTTASDWAWGVTLINE 841
 Db 685 ENLVKIGPGMSRDVYSTDYRVGHTMLPIRWPESIMRFTTESDWSLGVLNE 745
 Qy 842 VMLCRAQFGQLDQEVENAGEFRDQGRQVLSRPPACPOGYELMURCWSRESE 901
 Db 746 IFTYGR-QPWQLSNNEVTECI----TQGR--VLRQRPICPQEVEYLUGCGWOREPHMR 797
 Qy 902 PPFSOLHRL 911
 Db 798 KNTKGINTL 807

RESULT 14
 A55178 neurotrophin receptor trkC precursor - human
 C;Species: Homo sapiens (man)
 C;Accession: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Jun-1999
 C;Accession: A55178
 C;McGregor, L.M.; Baylin, S.B.; Griffin, C.A.; Hawkins, A.L.; Nelkin, B.D.
 Genomics 22, 267-272, 1994
 A;Title: Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal assignment
 A;Reference number: A55178; MUID:95104834
 A;Accession: A55178
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-825 <MCG>
 A;Cross-references: GB:U05012; NID:9442389; PIDN: AAA75374.1; PID:9442390
 C;Genetics:
 A;Gene: GDB:WTRK3
 A;Cross-references: GDB:122899; OMIM: 191316
 A;Map position: 13q24-15q25
 C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glyc
 C;Keywords: alternative splicing; ATP; growth factor receptor
 F;79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
 F;104-107/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
 F;128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F;151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
 F;536-817/Domain: protein kinase homology <KIN>
 F;544-552/Region: Protein kinase ATP-binding motif

Query Match 13.0%; Score 641.5.; DB 2; Length 825;
 Best Local Similarity 32.5%; Pred. No. 3.8e-22;
 Matches 174; Conservative 67; Mismatches 131; Indels 163; Gaps 19;

Db 490 RGNPHPSACVPMG-----SALLSNPA-----YRLLATYAR 522
 Qy 526 RGNPHPSACVPMG-----SALLSNPA-----YRLLATYAR 522
 Db 326 RGNPHPSACVPMG-----SALLSNPA-----YRLLATYAR 522
 Qy 523 PRPGPGPPTPAWAKPTNQAYSDYME--PERFGAPL---PPPRNSVPHYAADV 575
 Db 382 NPLG-----TANQITNGHFLKEPPPESTDNFILFDEVSPTPPIVTHKPEDTF 430
 Qy 576 TIQGVTSQNTYAVP-----P 592

Db 431 GYSTAVGLAFAVCLVLFMINKYGRSKRMKGPKIVAVISEEDSASPLHHINHGTT 490
 Qy 593 PGAVGDGP-----PRVDEP-----RSRLPKKEKGEGOF 622
 Db 491 PESLDAGDPDTWVIGMTRIPVIENPOVYRQGHNCHKPDTYQHKKRDRDILVKRLBGEAFG 550
 Qy 623 EYHLCEDVSPQDLVSLDPLPNTRKGHPILVAVKILRDPDKTNAFSLSFRNPLKEYKIM 682
 Db 551 KVFLAEC-----YNLSFTK-DKMLVAVKALK-DPT----LAARKDFOREELL 592
 Qy 683 SRLKDPNPNIRLGLGVQDDPLCMITDYMENGDLNQFSAHQLEDAKAEGAPG----DGQ 737

Db	593	TNLQEHVIVKRYGVGGDGPFLIMVYMKHQDLNKRFLRAH-----	-GPNAAMILVDGQ	643
Qy	738	AAQGP-TISYPMLLHVAAQTASGMRLATLNFVRDLATRNLGVENFTIKADGMSRN	796	
Db	644	PROAKGELGIQSQMLHTASQATSGMVLASOFVHQLATRNLGVANLVLIGDRMSRD	703	
Qy	797	LYADGYRVRGCRAVLPIRMAWECILMGKTTASDWAGYLWEVLMCRAQPFGQLTD	856	
Db	704	VYSTDYVRVGHTMLPIRWHPPESMYRKTTESDWGFCVILWEIFTYK-QPWFQLSN	762	
Qy	857	EQVLENAGEFRDQGRQQVYISRRPPACPQGKYLEMLRCWSEBSEORPPFSOLHRL	911	
Db	763	TEVIECI----TQGR--VLERPRVCPKEVYDVMLGCWQREPQQRNLNIKSIYKIL	810	
RESULT	15		'1	
TYR7TB				
N;Alternate names: receptor tyrosine kinase tira				
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)				
C;Species: Rattus norvegicus (Norway rat)				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-2000				
C;Accession: A41981				
R;Maekin, S.O.; Suier, U.; Drinkwater, C.C.; Welcher, A.A.; Shooter, E.M.				
Proc. Natl. Acad. Sci. U.S.A., 89, 2374-2378, 1992				
A;Title: The rat trk protooncogene product exhibits properties characteristic of the sld				
A;Reference number: A41981; MUID:92196121				
A;Accession: A41981				
A;Molecule type: mRNA				
A;Residues: 1-799 <MEA>				
A;Cross-references: GB:M85214; NID:9207481; PID:AAA42286.1; PID:9207482				
A;Note: sequence extracted from NCBI backbone (NCBINR88433, NCBIPI88343)				
C;Comment: The proto-oncogene trka is activated by gene fusion. The amino end of several				
C;Function:				
A;Description: regulation of nervous system development; receptor for nerve growth factor; superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycoprotein kinase				
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprotein				
F1-32;domain: signal sequence #status predicted <SIG>				
F1-33-799;product: nerve growth factor receptor, high-affinity #status predicted <MAT>				
F1-33-424;domain: extracellular #status predicted <EXT>				
F1-67-91;domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>				
F1-92-115;domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>				
F1-116-138;domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>				
F1-139-150;domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR>				
F1-425-441;domain: transmembrane #status predicted <TM>				
F1-442-799;domain: cytosolic #status predicted <CYT>				
F1-511-791;domain: protein kinase homology <Kin>				
F1-519-527;Region: protein kinase ATP-binding motif				
F1-671-1211;190-204,255,264,320,325,341,361,404;Binding site: carbohydrate (Asn) (covalent)				
F1-547;binding site: Lys #status predicted <Covalent>				
F1-683;binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted				
F1-794;binding site: phosphate (Tyr) (covalent) #status predicted				
Query Match	13.0%	Score 640.5; DB 1; Length 799;		
Best Local Similarity	29.5%	Pred. No. 4e-22; DB 1;		
Matches	190;	Conservative 78; Mismatches 155; Indels 221; Gaps 22;		
Qy	335	SYPLGLGRVARFLQ-----RLFLAGPWLFSEISPI-----	365	
Db	289	SVHLGKAVEQHWCICPPSVDFGQAPSRLWFFNGS---VNLNTSRIFTQFLESALTNETMRH	346	
Qy	366	-----SDVWNSSPAPALGTP-----PAPWWPPGPPPTNTSSLETPR	403	
Db	347	GCLRLNQPTFHVNNGNTLLAANPYQQAASIMAFAFMONPFPNPDPIPVSFSPVDTNST	406	
Qy	404	GOOPVAKAEGSPTTAILGCLVATILLIALLMLWRLHWRLLSKERR-----V	454	
Db	407	SRDPEVKDEPPFGVSVAVGLAASAIFL-SALL-----VLNKGQRSKFGINPAV	458	